

OIIPE

(2)

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/826,752

DATE: 04/30/2001
 TIME: 11:04:49

Input Set : A:\0050.1491-005.TXT
 Output Set: N:\CRF3\04302001\I826752.raw

p.5

ENTERED

4 <110> APPLICANT: Guarente, Leonard P.
 5 Austriaco Jr., Nicanor
 6 Claus, James J.
 7 Cole, Francesca
 8 Kennedy, Brian
 11 <120> TITLE OF INVENTION: GENES DETERMINING CELLULAR SENESCENCE IN
 12 YEAST
 14 <130> FILE REFERENCE: 0050.1491-005
 C--> 16 <140> CURRENT APPLICATION NUMBER: US/09/826,752
 C--> 16 <141> CURRENT FILING DATE: 2001-04-05
 16 <150> PRIOR APPLICATION NUMBER: US 08/396,001
 17 <151> PRIOR FILING DATE: 1995-02-28
 19 <150> PRIOR APPLICATION NUMBER: PCT/US94/09351
 20 <151> PRIOR FILING DATE: 1994-08-15
 22 <150> PRIOR APPLICATION NUMBER: US 08/107,408
 23 <151> PRIOR FILING DATE: 1993-08-16
 25 <150> PRIOR APPLICATION NUMBER: US 09/323,433
 26 <151> PRIOR FILING DATE: 1999-06-01
 28 <160> NUMBER OF SEQ ID NOS: 48
 30 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 32 <210> SEQ ID NO: 1
 33 <211> LENGTH: 1946
 34 <212> TYPE: DNA
 35 <213> ORGANISM: Saccharomyces cerevisiae
 37 <220> FEATURE:
 38 <221> NAME/KEY: CDS
 39 <222> LOCATION: (322)...(1671)
 40 <223> OTHER INFORMATION: UTH1
 42 <400> SEQUENCE: 1
 43 tgaaaaagtg gaactagacc ccacgtcagc gggcctaggc ccttcaatgt gttagaatac 60
 44 acagcgtgcc tagttcctgg tgcctggatc tcgaggccgc ggcactggaa aagcccttc 120
 45 ttttccagat cgggaaacct aatgagtcca taaaaagaaa ttagagggtg gtgttgacgt 180
 46 ttgcccgtt ttgggcaagt aggtctttct gcacggcccg gcccggtcg tgcggaaaaa 240
 47 gaaaaaagca gacaaaacaa aatttttctt ttttttcgcc ttgtttctc ctgattcggg 300
 48 tatataagtg aataccatct a atg tgt ttc ctt ctc gag acc tcg gcg tct 351
 49 Met Cys Phe Leu Leu Glu Thr Ser Ala Ser
 50 1 5 10
 52 ccc aga tca aag ctc agc aaa gat ttt aaa ccg caa ttt acg ctc ctt 399
 53 Pro Arg Ser Lys Leu Ser Lys Asp Phe Lys Pro Gln Phe Thr Leu Leu
 54 15 20 25
 56 tca tcg gta act aag aag aaa aaa aaa gta cga cca cac aat ttc 447
 57 Ser Ser Val Thr Lys Lys Lys Lys Lys Lys Val Arg Pro His Asn Phe
 58 30 35 40
 60 cag tgt att cat tcc tta aac ttc gtt tat ttt tta ttc att cat tca 495
 61 Gln Cys Ile His Ser Leu Asn Phe Val Tyr Phe Leu Phe Ile His Ser
 62 45 50 55
 64 ttt tta ttt gaa tat aac caa cta cta gtc ctt cct tta aac aaa aat 543

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65 Phe Leu Phe Glu Tyr Asn Gln Leu Leu Val Leu Pro Leu Asn Lys Asn
66      60      65      70
68 tta ccc tcc ctt aat ttt tca aga aat tcc agt atg aaa tta tcc gct 591
69 Leu Pro Ser Leu Asn Phe Ser Arg Asn Ser Ser Met Lys Leu Ser Ala
70 75      80      85      90
72 cta tta gct tta tca gcc tcc acc gcc gtc ttg gcc gct cca gct gct 639
73 Leu Leu Ala Leu Ser Ala Ser Thr Ala Val Leu Ala Ala Pro Ala Val
74      95      100      105
76 cac cat agt gac aac cac cac cac aac gac aag cgt gcc gtt gtc acc 687
77 His His Ser Asp Asn His His His Asn Asp Lys Arg Ala Val Val Thr
78      110      115      120
80 gtt act cag tac gtc aac gca gac ggc gct gtt gtt att cca gct gcc 735
81 Val Thr Gln Tyr Val Asn Ala Asp Gly Ala Val Val Ile Pro Ala Ala
82      125      130      135
84 acc acc gct acc tcg gcg gct gct gat gga aag gtc gag tct gtt gct 783
85 Thr Thr Ala Thr Ser Ala Ala Ala Asp Gly Lys Val Glu Ser Val Ala
86      140      145      150
88 gct gcc acc act act ttg tcc tcg act gcc gcc gcc gct act acc tct 831
89 Ala Ala Thr Thr Thr Leu Ser Ser Thr Ala Ala Ala Ala Thr Thr Ser
90 155      160      165      170
92 gcc gcc gcc tct tct tcc tcc tct tcc tct tcc tcc tct tcc tct tct 879
93 Ala Ala Ala Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser
94      175      180      185
96 tcc tct gtt ggt tct gga gat ttt gaa gat ggt acc att tcc tgt tct 927
97 Ser Ser Val Gly Ser Gly Asp Phe Glu Asp Gly Thr Ile Ser Cys Ser
98      190      195      200
100 gat ttc cca tcc gga caa ggt gct gtc tcc ttg gac tgg tta ggt cta 975
101 Asp Phe Pro Ser Gly Gln Gly Ala Val Ser Leu Asp Trp Leu Gly Leu
102      205      210      215
104 ggc ggc tgg gct tcc atc atg gac atg aac ggt aac acc gcc acc tct 1023
105 Gly Gly Trp Ala Ser Ile Met Asp Met Asn Gly Asn Thr Ala Thr Ser
106      220      225      230
108 tgt caa gac gga tac tac tgt tct tac gct tgt tct cca ggt tac gct 1071
109 Cys Gln Asp Gly Tyr Tyr Cys Ser Tyr Ala Cys Ser Pro Gly Tyr Ala
110 235      240      245      250
112 aag acc caa tgg cct tct gaa caa cct tcc gat ggt aga tcc gtt ggt 1119
113 Lys Thr Gln Trp Pro Ser Glu Gln Pro Ser Asp Gly Arg Ser Val Gly
114      255      260      265
116 ggt tta tac tgt aag aac ggt aaa tta tac cgt tcc aac acc gac act 1167
117 Gly Leu Tyr Cys Lys Asn Gly Lys Leu Tyr Arg Ser Asn Thr Asp Thr
118      270      275      280
120 aac agt ttg tgt gta gaa ggt caa ggc tct gct caa gct gtt aac aag 1215
121 Asn Ser Leu Cys Val Glu Gly Gln Gly Ser Ala Gln Ala Val Asn Lys
122      285      290      295
124 gtc tcc ggc tcc att gct atc tgt ggt acc gat tat cca ggt tct gaa 1263
125 Val Ser Gly Ser Ile Ala Ile Cys Gly Thr Asp Tyr Pro Gly Ser Glu
126      300      305      310
128 aac atg gtc gtt cct acc gta gtt ggc gct ggt tcc tcc caa cca atc 1311
129 Asn Met Val Val Pro Thr Val Val Gly Ala Gly Ser Ser Gln Pro Ile

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130 315          320          325          330
132 aac gtc atc aag gag gac tcc tac tat caa tgg caa ggt aag aag acc 1359
133 Asn Val Ile Lys Glu Asp Ser Tyr Tyr Gln Trp Gln Gly Lys Lys Thr
134          335          340          345
136 tct gcc caa tac tac gtt aac aac gct ggt gtc tct gtg gaa gat ggt 1407
137 Ser Ala Gln Tyr Tyr Val Asn Asn Ala Gly Val Ser Val Glu Asp Gly
138          350          355          360
140 tgt atc tgg ggt act gag ggt tcc ggt gtc ggt aac tgg gcc cca gtt 1455
141 Cys Ile Trp Gly Thr Glu Gly Ser Gly Val Gly Asn Trp Ala Pro Val
142          365          370          375
144 gtc ttg ggt gct ggt tac act gat ggt atc act tac ttg tcc atc att 1503
145 Val Leu Gly Ala Gly Tyr Thr Asp Gly Ile Thr Tyr Leu Ser Ile Ile
146          380          385          390
148 cca aac cca aac aac aaa gaa gca cca aac ttt aac atc aag atc gtt 1551
149 Pro Asn Pro Asn Asn Lys Glu Ala Pro Asn Phe Asn Ile Lys Ile Val
150 395          400          405          410
152 gcc acc gat ggc tct acc gtc aat ggt gct tgc tct tac gaa aat ggt 1599
153 Ala Thr Asp Gly Ser Thr Val Asn Gly Ala Cys Ser Tyr Glu Asn Gly
154          415          420          425
156 gtc tac tct ggc tct ggc tct gac ggt tgt act gtt tca gtt act tct 1647
157 Val Tyr Ser Gly Ser Gly Ser Asp Gly Cys Thr Val Ser Val Thr Ser
158          430          435          440
160 ggt tct gct aac ttt gtc ttc tac taggcctttt ttccttgaat attgcaaata 1701
161 Gly Ser Ala Asn Phe Val Phe Tyr
162          445          450
164 agctttttgct agtacttttt ttactccggt cattttatgg tttatttttc aattagttcg 1761
165 tttttccaca atacaaaaaa acacagtcct ttgtactatc ccttttattt cattattttt 1821
166 tcttttttaa gataccacta gatattatca tatatagcat attatataac ataaaaagtc 1881
167 aagaaaaaaa atgtttttat cactttctat aactgcatat ctttttttgc atttcgaatg 1941
168 attgc 1946
170 <210> SEQ ID NO: 2
171 <211> LENGTH: 450
172 <212> TYPE: PRT
173 <213> ORGANISM: Saccharomyces cerevisiae
175 <220> FEATURE:
176 <221> NAME/KEY: VARIANT
177 <222> LOCATION: (1)...(441)
178 <223> OTHER INFORMATION: Xaa = Any Amino Acid
180 <400> SEQUENCE: 2
181 Met Cys Phe Leu Leu Glu Thr Ser Ala Ser Pro Arg Ser Lys Leu Ser
182 1 5 10 15
183 Lys Asp Phe Lys Pro Gln Phe Thr Leu Leu Ser Ser Val Thr Lys Lys
184 20 25 30
185 Lys Lys Lys Lys Val Arg Pro His Asn Phe Gln Cys Ile His Ser Leu
186 35 40 45
187 Asn Phe Val Tyr Phe Leu Phe Ile His Ser Phe Leu Phe Glu Tyr Asn
188 50 55 60
189 Gln Leu Leu Val Leu Pro Leu Asn Lys Asn Leu Pro Ser Leu Asn Phe
190 65 70 75 80

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191 Ser Arg Asn Ser Ser Met Lys Leu Ser Ala Leu Leu Ala Leu Ser Ala
192      85      90      95
193 Ser Thr Ala Val Leu Ala Ala Pro Ala Val His His Ser Asp Asn His
194      100      105      110
195 His His Asn Asp Lys Arg Ala Val Val Thr Val Thr Gln Tyr Val Asn
196      115      120      125
197 Ala Asp Gly Ala Val Val Ile Pro Ala Ala Thr Thr Ala Thr Ser Ala
198      130      135      140
199 Ala Ala Asp Gly Lys Val Glu Ser Val Ala Ala Thr Thr Thr Leu
200 145      150      155      160
201 Ser Ser Thr Ala Ala Ala Thr Thr Ser Ala Ala Ala Ser Ser Ser
202      165      170      175
203 Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Val Gly Ser Gly
204      180      185      190
205 Asp Phe Glu Asp Gly Thr Ile Ser Cys Ser Asp Phe Pro Ser Gly Gln
206      195      200      205
207 Gly Ala Val Ser Leu Asp Trp Leu Gly Leu Gly Gly Trp Ala Ser Ile
208      210      215      220
209 Met Asp Met Asn Gly Asn Thr Ala Thr Ser Cys Gln Asp Gly Tyr Tyr
210 225      230      235      240
211 Cys Ser Tyr Ala Cys Ser Pro Gly Tyr Ala Lys Thr Gln Trp Pro Ser
212      245      250      255
213 Glu Gln Pro Ser Asp Gly Arg Ser Val Gly Gly Leu Tyr Cys Lys Asn
214      260      265      270
215 Gly Lys Leu Tyr Arg Ser Asn Thr Asp Thr Asn Ser Leu Cys Val Glu
216      275      280      285
217 Gly Gln Gly Ser Ala Gln Ala Val Asn Lys Val Ser Gly Ser Ile Ala
218      290      295      300
219 Ile Cys Gly Thr Asp Tyr Pro Gly Ser Glu Asn Met Val Val Pro Thr
220 305      310      315      320
221 Val Val Gly Ala Gly Ser Ser Gln Pro Ile Asn Val Ile Lys Glu Asp
222      325      330      335
223 Ser Tyr Tyr Gln Trp Gln Gly Lys Lys Thr Ser Ala Gln Tyr Tyr Val
224      340      345      350
225 Asn Asn Ala Gly Val Ser Val Glu Asp Gly Cys Ile Trp Gly Thr Glu
226      355      360      365
227 Gly Ser Gly Val Gly Asn Trp Ala Pro Val Val Leu Gly Ala Gly Tyr
228      370      375      380
229 Thr Asp Gly Ile Thr Tyr Leu Ser Ile Ile Pro Asn Pro Asn Asn Lys
230 385      390      395      400
231 Glu Ala Pro Asn Phe Asn Ile Lys Ile Val Ala Thr Asp Gly Ser Thr
232      405      410      415
233 Val Asn Gly Ala Cys Ser Tyr Glu Asn Gly Val Tyr Ser Gly Ser Gly
234      420      425      430
235 Ser Asp Gly Cys Thr Val Ser Val Thr Ser Gly Ser Ala Asn Phe Val
236      435      440      445
237 Phe Tyr
238      450
241 <210> SEQ ID NO: 3

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242 <211> LENGTH: 3455
243 <212> TYPE: DNA
244 <213> ORGANISM: Saccharomyces cerevisiae
246 <220> FEATURE:
247 <221> NAME/KEY: CDS
248 <222> LOCATION: (663)...(3164)
249 <223> OTHER INFORMATION: UTH4
251 <400> SEQUENCE: 3
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253 gatcagccta tcgacacgcc ttttttagcg gtctaacaat ctccgtttat gtcgtatgga 120
254 attttctatac ttgaccctac cttatttctc gaatatgcct ataaggattt tctcgaaaga 180
255 agggcttcgg gaaagaggcg cctcaggcaa aaatgagcaa aaaaaaaaaa aaaaagaaaa 240
256 gattcgaaga tctatgaaaa atttatgcag attcgttgag agttataagg attttactct 300
257 ttatggttat aggtttcatt ctaaaatcaa gcataaattt tgtgttttgt cttcctcttt 360
258 tcctgtcctc ttttttgcc atcctctgtc gccattgaag tcgaacttta tagatagatt 420
259 tactcttgat tctcagcat ctcaggccac ctggacactg tacatggttg tgattgttct 480
260 ctttctcagt tatcgaaatt gatcctaggc ttatactcca aaatcggctc tgcacacgcc 540
261 ttatttttgt ggtttcactt tactaacaca acattctttt attcaatcag atcaataacg 600
262 aaccatttcc atctgccgac tcagcatcga ttttaactac gtctacatca aataactcct 660
263 ta atg tct tac aat cat cag cct caa cta tct att aac tcc gtc caa 707
264 Met Ser Tyr Asn His Gln Pro Gln Leu Ser Ile Asn Ser Val Gln
265 1 5 10 15
266 tca ctc ttg gag ccc gtg acc cct ccg cct ttg ggc cag atg aat aac 755
267 Ser Leu Leu Glu Pro Val Thr Pro Pro Pro Leu Gly Gln Met Asn Asn
268 20 25 30
269 aaa aga aac cat caa aag gct cat tcg ctt gat ctc tct ggt ttt aat 803
270 Lys Arg Asn His Gln Lys Ala His Ser Leu Asp Leu Ser Gly Phe Asn
271 35 40 45
272 cag ttc ata tca tcg aca caa tct ccc ttg gct ttg atg aat aat aca 851
273 Gln Phe Ile Ser Ser Thr Gln Ser Pro Leu Ala Leu Met Asn Asn Thr
274 50 55 60
275 tca aca tcg aat tct gct aac tct ttt tcc ccg aat cct aat gct gct 899
276 Ser Thr Ser Asn Ser Ala Asn Ser Phe Ser Pro Asn Pro Asn Ala Ala
277 65 70 75
278 agc aac tcc act ggg ctt tca gcc tca atg gca aat cct cca gcc att 947
279 Ser Asn Ser Thr Gly Leu Ser Ala Ser Met Ala Asn Pro Pro Ala Ile
280 80 85 90 95
281 cta cca tta atc aat gag ttt gat ctg gaa atg gat ggt ccc agg aga 995
282 Leu Pro Leu Ile Asn Glu Phe Asp Leu Glu Met Asp Gly Pro Arg Arg
283 100 105 110
284 aaa tca agc cac gat ttc acg gtt gtt gct cct tcg aac tct ggt gtc 1043
285 Lys Ser Ser His Asp Phe Thr Val Val Ala Pro Ser Asn Ser Gly Val
286 115 120 125
287 aat acc tcc agt tta att atg gaa aca cca tcc tct tca gtg act cct 1091
288 Asn Thr Ser Ser Leu Ile Met Glu Thr Pro Ser Ser Ser Val Thr Pro
289 130 135 140
290 gct gca tct ctc aga aat ttt agc aat agt aat aat gct gct tcc aaa 1139
291 Ala Ala Ser Leu Arg Asn Phe Ser Asn Ser Asn Ala Ala Ser Lys
292 145 150 155

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Please Not :

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequenc Listing to ensure that a corresp nding explanation is presented in the <220> to <223> fields of each sequence which pres nts at least one n r Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/826,752

DATE: 04/30/2001

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Input Set : A:\0050.1491-005.TXT

Output Set: N:\CRF3\04302001\I826752.raw

L:16 M:270 C: Current Application Number differs, Replaced Current Application No
L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:2103 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:2105 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:2107 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:2109 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:2111 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:2113 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:2115 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:2117 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:2119 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:2121 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15